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IN THE SPECIFICATION:

Please amend the paragraph at page 7, lines 5-7 as follows:

Figure 2 shows the complete protein (SEQ ID NO:5) encoded by the nucleotide sequence given in Figure 1. The predicted amino acid sequence (SEQ ID NO:2) and signal sequence (SEQ ID NO:3) based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1), wherein the signal sequence is indicated as bolded.

Please amend the paragraph at page 19, lines 3-8 as follows:

A Basic BLASTN search (www.ncbi.nlm.nih.gov/BLAST) of the non-redundant nucleic acid sequence database was conducted on September 12, 2001, with the *eg/8* gene sequence presented in Figure 1 (SEQ ID NO:1), indicated that the only sequences producing significant alignments (i.e. with an E value of less than 10^{-5}) were GenBank Accession Number S45137 (CMC1, carboxymethylcellulase of *Cryptococcus flavus*).

Please amend the paragraph at page 24, lines 15-24 as follows:

A Basic BLASTP search (www.ncbi.nlm.nih.gov/BLAST) of the non-redundant protein database, conducted on September 12, 2001 with the EGVIII amino acid sequence indicated 52% identity with GenBank Accession Number AB021657 (endoglucanase II of *Trichoderma viride*), 51% sequence identity to GenBank Accession Number M19373 (endoglucanase EG-II precursor of *Trichoderma reesei*), 50% sequence identity to GenBank Accession Number X89564 (endoglucanase 2 of *Penicillium janthinellum*), and 52% sequence identity to GenBank Accession Number U13914 (endo-beta-1,4-glucanase of *Macrophomina phaseolina*). These sequence similarities indicate that EGVIII is a member of glycosyl hydrolase family 5 (Henrissat, B. and Bairoch, A. (1993) *Biochem. J.* 293:781-788).

Please amend the paragraph at page 29, lines 1-5 as follows:

Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; "www.atcc.org/"). After fungal growth has been established, the cells are exposed to conditions effective to cause or permit the over expression of EGVIII.

Please amend the paragraph at page 37, lines 21-25 as follows:

Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, e.g., BLASTN,

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BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at
www.ncbi.nlm.nih.gov/BLAST/. See also, Altschul, *et al.*, 1990 and Altschul, *et al.*, 1997.

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